

CGCTATCCCTCCCTCGTACAAACGCAAGAGCAGCAATGGCCGCTCCAGAAGTACACG 60  
M A V Q K Y T  
-25  
GTGGCTCTATTCCCTCGCCGCTGGCCCTCGTGGCGGGCCCGCCGCTCCTACGCCGCTGAC 120  
V A L F L A V A L V A G P A A S Y A A D  
-15  
GCCGGCTACACCCCGCAGCCGCGGCCACCCCGGCTACTCCTGTGCTGCCACCCCGGCTGCG 180  
A G Y T P A A A A T P A T P A A A  
-10  
GCTGGAGGGAAGCGACGACCGAGCAGCAGCAAGCTGCTGGAGGACGTCAACGCTGGCTTC 240  
A G G K A T T D E Q K L L E D V N A G F  
-5  
AAGCAGCCGCTGGCCGCGCTGCCAACGCCCTCCGGCGGACAAAGTTCAAGATCTTCGAG 300  
K A A V A A A A N A P P A D K F K I F E  
-20  
GCCGCCCTTCTCCGAGTCCCAAGGGCTCCTCGCCACCTCCGCCGCAAGCACCCTGGC 360  
A A F S E S S K G L L A T S A A K A P G  
-25  
CTCATCCCCAAGCTCGACACCGCTACGACGTGCGCTACAAGCGCGCGGCGCCACC 420  
L I P K L D T A Y D V A Y K A A E G A T  
-30  
CCCGAGGCCAAGTACGACGCTTCTGCTCACTGCCCTCACCGAAGCGCTCCGCTCATCGCC 480  
P E A K Y D A F V T A L T E A L R V I A  
-35  
GGCGCCCTCGAGTCCAGCGCTCAAGCCCGCCACCGAGGAGGTCCCTGCTAAGATC 540  
G A L E V H A V K P A T E E V P A A K I  
-40  
125

Fig. 1

CCACCGGTGAGCTGCAGATCGTTGACAAGATCGATGCTGCCTTCAAGATCGAGCCACC 600  
 P T G E L Q I V D K I D A A F K I A A T  
 145 150 155 160  
 CCGCCAAACGGCGCCCCACCAACGATAAGTTCACCGTCTTCGAGAGTGCCCTTCAACAAG 660  
 A A N A A P T N D K F T V F E S A F N K  
 165 170 175 180  
 CCTCAATGAGTGACGGCGCGCCTATGAGACCTACAAGTTCATCCCTCCCTCGAG 720  
 A L N E C T G G A Y E T Y K F I P S L E  
 185 190 195 200  
 CCGCGGTCAAGCAGGCCCTACGCCGCCACCGTCCGCCGCCGAGGTCAAGTACGCC 780  
 A A V K Q A Y A A T V A A A P E V K Y A  
 205 210 215 220  
 TCTTTGAGGCGCGCTGACCAAGGCCATCACCGCCATGACCCAGGCACAGAGGCCGGC 840  
 V F E A A L T K A I T A M T Q A Q K A G  
 225 230 235 240  
 AACCCGCTGCCGCGCTGCCACAGCGCGCAACCGTTGCCACCGCGCGCCGCAACCGCC 900  
 K P A A A A T G A A T V A T G A A T A  
 245 250 255 260  
 CCGCGGTGCTGCCACCGCGCTGCTGGTGGCTACAAAGCCTGATCAGCTTGCTAATAT 960  
 A A G A A T A A G G Y K A \*  
 265 270 275  
 CTACTGAACGTATGTGATGATCCGGCGCGGAGTGGTTTGTGATAATTAATC 1020  
 TCGTTTTCGTTTCATGCAGCCGCGATCGAGAGGGCTTGCTGCTGTAATAATCAATA 1080  
 TTTTCATTTCTTTTGAATCTGTAAATCCCCATGACAAAGTAGTGGATCAAGTCGGCAT 1140  
 TATCACCGTTGATGCGAGTTAACGATGGGAGTTTATCAAGAATTATTTATAAAAA 1200  
 AAAAAAATAAAAAAATAAAAAA 1229

Fig. 1 cont.

3/20

LIX-1    ADAGYTXAAAATXATXAATX  
LIX-1.1   ADAGYTPAAAATPATPAATP  
LIX-2    ATXATXAATXAAAAGGKATTD  
LIX-2.1   ATPATPAATPAAAGGKATTD  
LIX-3    AAAGGKATTDEQKLLEDVNA  
LIX-4    EQKLLEDVNAGFKAAVAAAA  
LIX-5    GFKAAVAAAAANAPPADKFKI  
LIX-6    NAPPADKFKIFEAAFSESSK  
LIX-7    FEAAFSESSKGLLATSAAKA  
LIX-8    GLLATSAAKAPGLIPKLDTA  
LIX-9    PGLIPKLDTAYDVAYKAAEG  
LIX-10   YDVAYKAAEGATPEAKYDAF  
LIX-11   ATPEAKYDAFVTALTEALRV  
LIX-12   VTALTEALRVIAGALEVHAV  
LIX-13   IAGALEVHAVKPATEEVPAA  
LIX-14   KPATEEVPAAKIPTGELQIV  
LIX-15   KIPTGELQIVDKIDAAFKIA  
LIX-16   DKIDAAFKIAATAANAAPT  
LIX-17   ATAANAAPTNDKFTVFESAF  
LIX-18   DKFTVFESAFNKKALNECTGG  
LIX-19   NKALNECTGGAYETYKFIPS  
LIX-20   AYETYKFIPSLEAAVKQAYA  
LIX-21   LEAAVKQAYAATVAAAPEVK  
LIX-22   ATVAAAPEVKYAVFEAALTK  
LIX-23   YAVFEAALTKAITAMTQAQK  
LIX-24   AITAMTQAQKAGKPAAAAAT  
LIX-25   AGKPAAAAATGAATVATGAA  
LIX-26   GAATVATGAATAAAGAATAA  
LIX-27   TAAAGAATAAAGGYKA

X REPRESENTS HYDROXYPROLINE RESIDUE

Fig. 2

08737904-110995

4/20

PEPTIDE NAME	PEPTIDE SEQUENCE
LPI-1	IAKVPPGPNITA EYGDKWLD
LPI-1.1	IAKVXPGXNITA EYGDKWLD
LPI-2	TAEYGDKWLD AKSTWYGKPT
LPI-3	AKSTWYGKPT GAGPKDNGGA
LPI-4	GAGPKDNGGACGYKNVDKAP
LPI-4.1	GAGPKDNGGACGYKDVDKAP
LPI-5	CGYKDVDKAPFNGMTGCGNT
LPI-6	FNGMTGCGNTPIFKDGRGCG
LPI-7	PIFKDGRGCGSCFEIKCTKP
LPI-8	SCFEIKCTKPESCSGEAVTV
LPI-9	ESCSGEAVTVTITDDNEEPI
LPI-10	TITDDNEEPIAPYHFDLSGH
LPI-11	APYHFDLSGHAFGSMADDGE
LPI-11.1	APYHFDLSGHAFGSMAKKGE
LPI-12	AFGSMADDGEEQKLR SAGEL
LPI-12.1	AFGSMAKKGEEQKLR SAGEL
LPI-13	EQKLR SAGELELQFRRVKCK
LPI-14	ELQFRRVKCKYPDDTKPTFH
LPI-15	YPDDTKPTFHVEKASNP NYL
LPI-16	VEKASNP NYLAILVKYVDGD
LPI-16.1	VEKGSNP NYLAILVKYVDGD
LPI-17	AILVKYVDGDGDVVAVDIKE
LPI-18	GDVVAVDIKEKGKDKWIELK
LPI-19	KGKDKWIELKESWGAVWRID
LPI-20	ESWGAVWRIDTPDKLTGPFT
LPI-21	TPDKLTGPFTVRYTTEGGTK
LPI-22	VRYTTEGGTKSEVEDVIPEG
LPI-23	SEVEDVIPEGWKADTSYS AK

Fig. 3

08/737904-112095

5/20

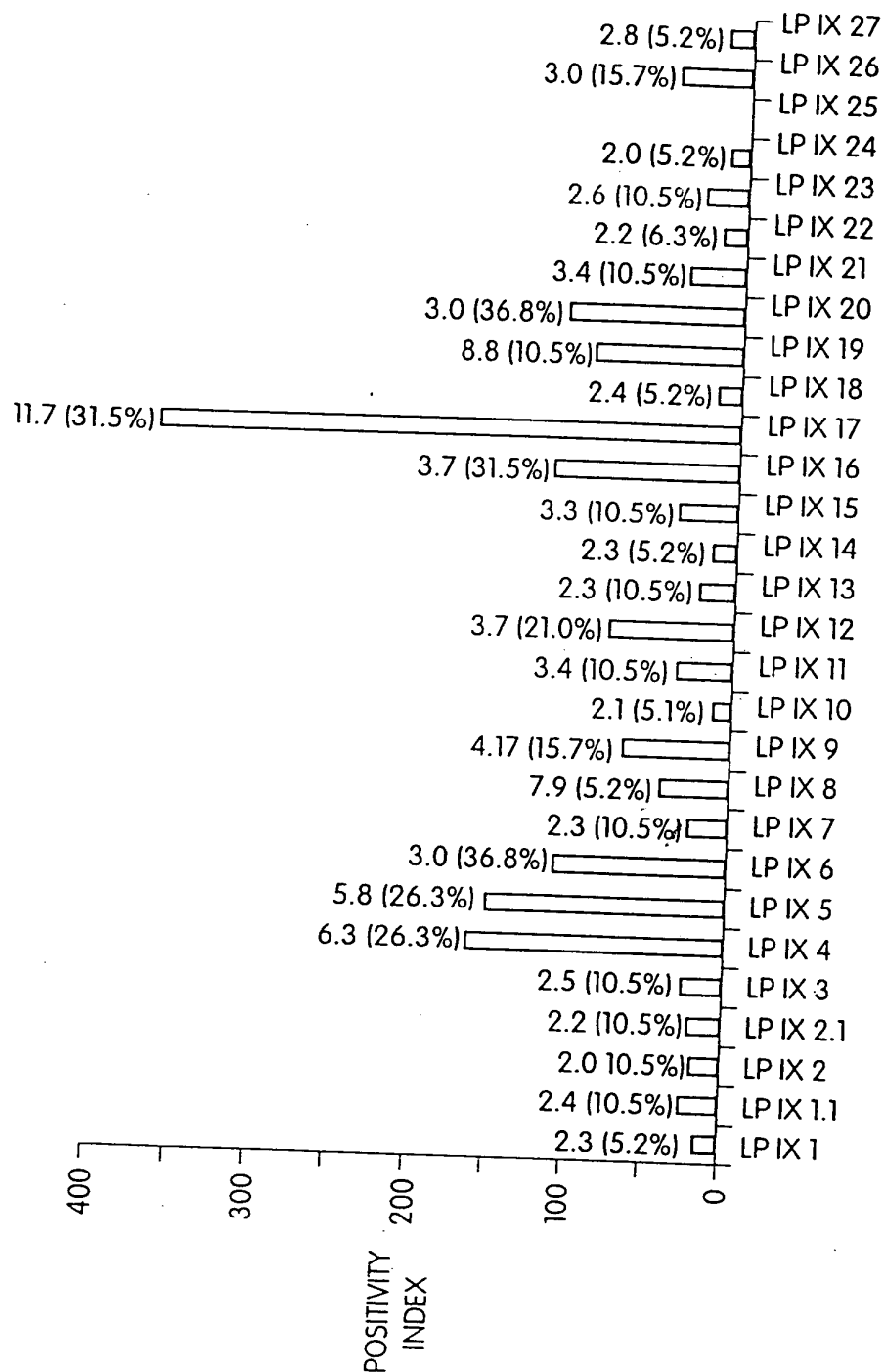


Fig. 4

960211-10645280

6/20

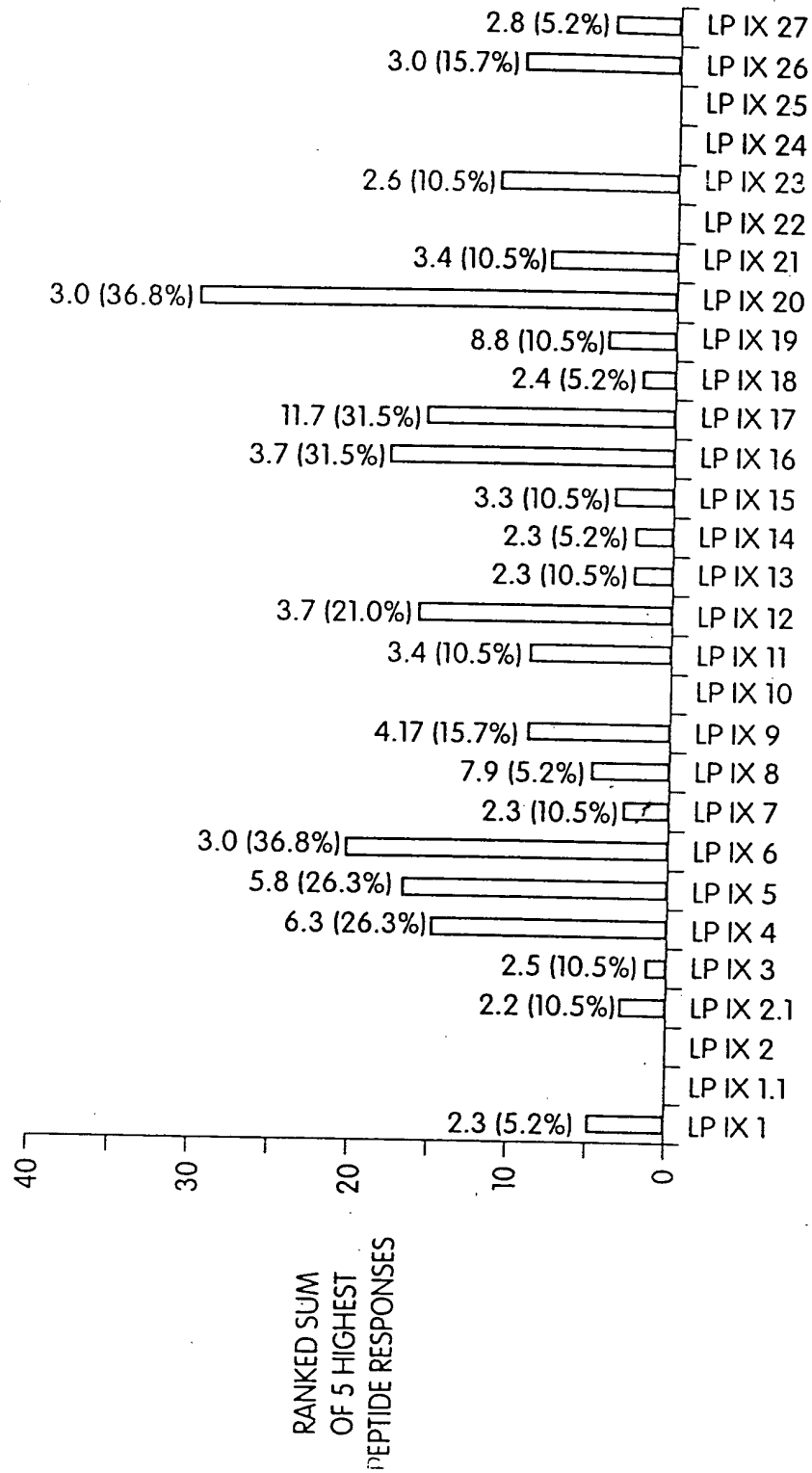


Fig. 5

08/737904 110628480

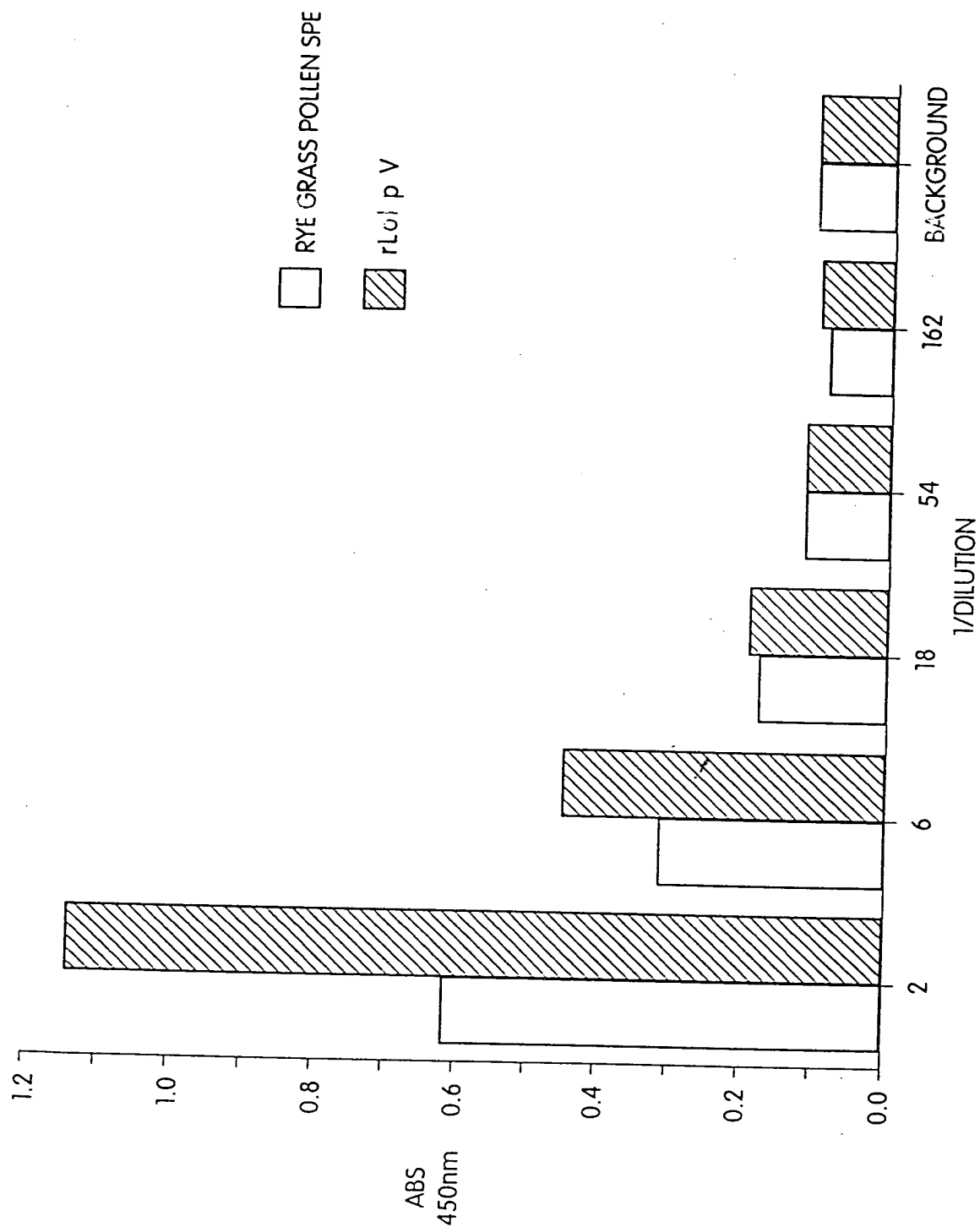


Fig. 6

8/20

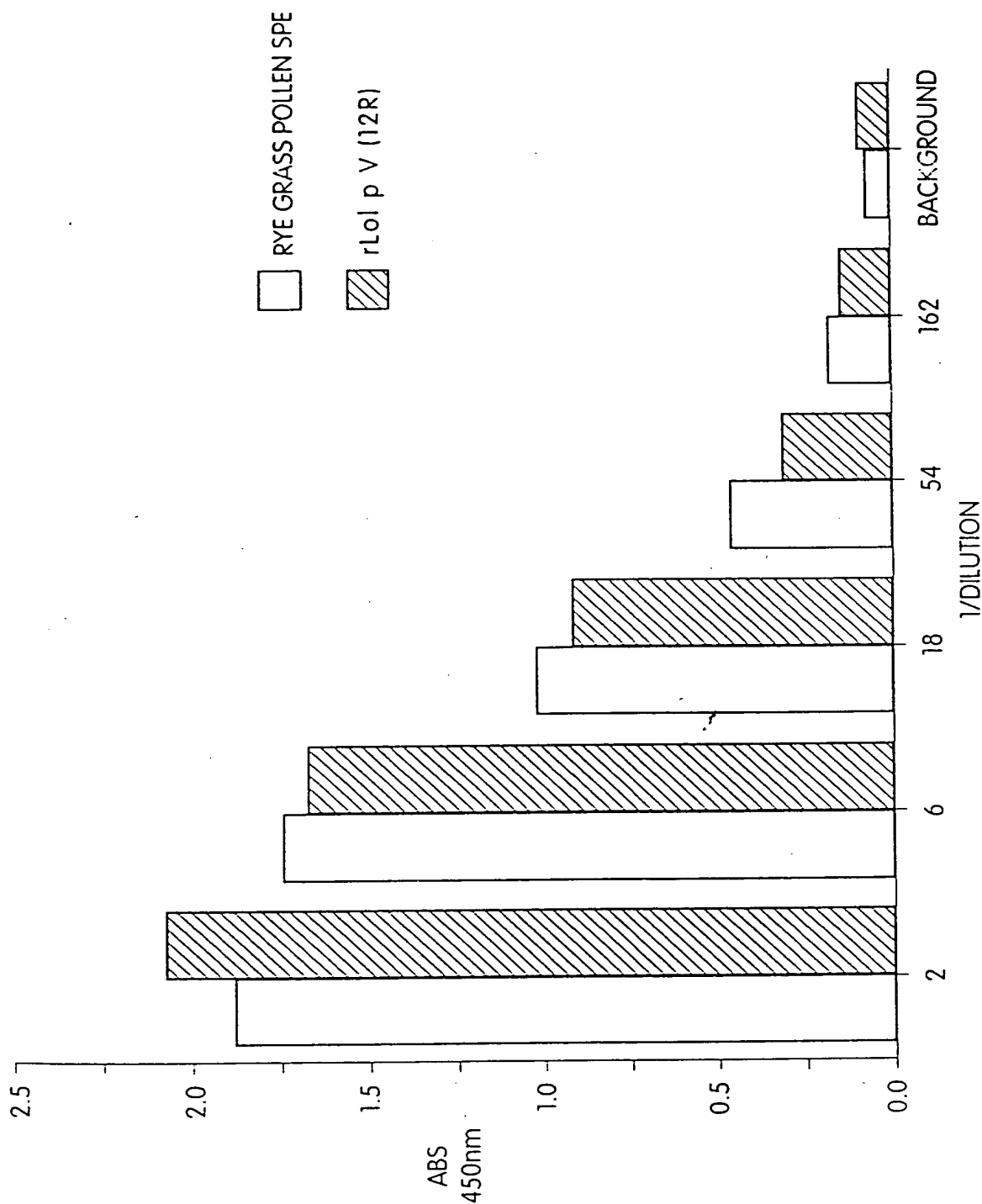


Fig. 7



9/20

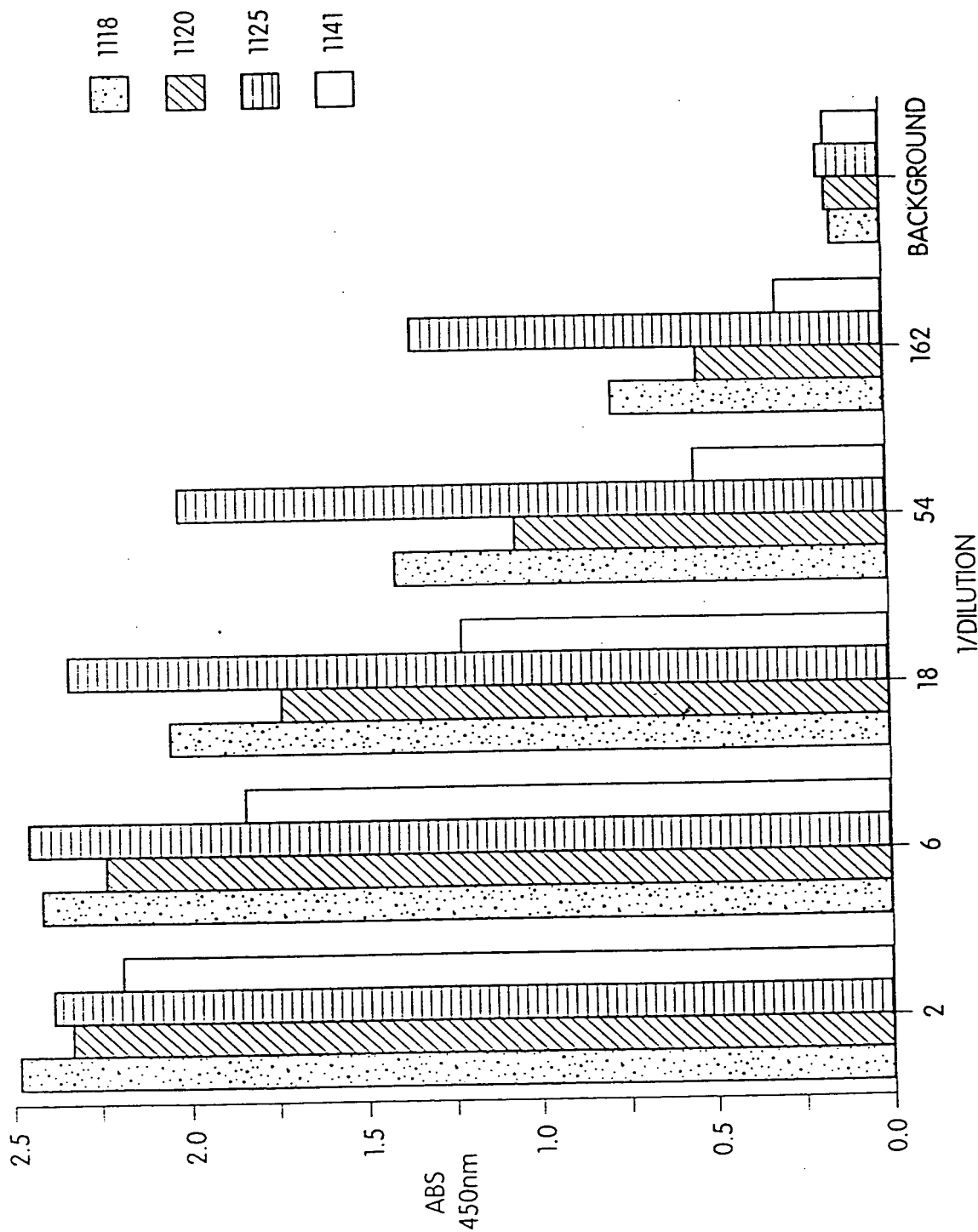


Fig. 8

10/20

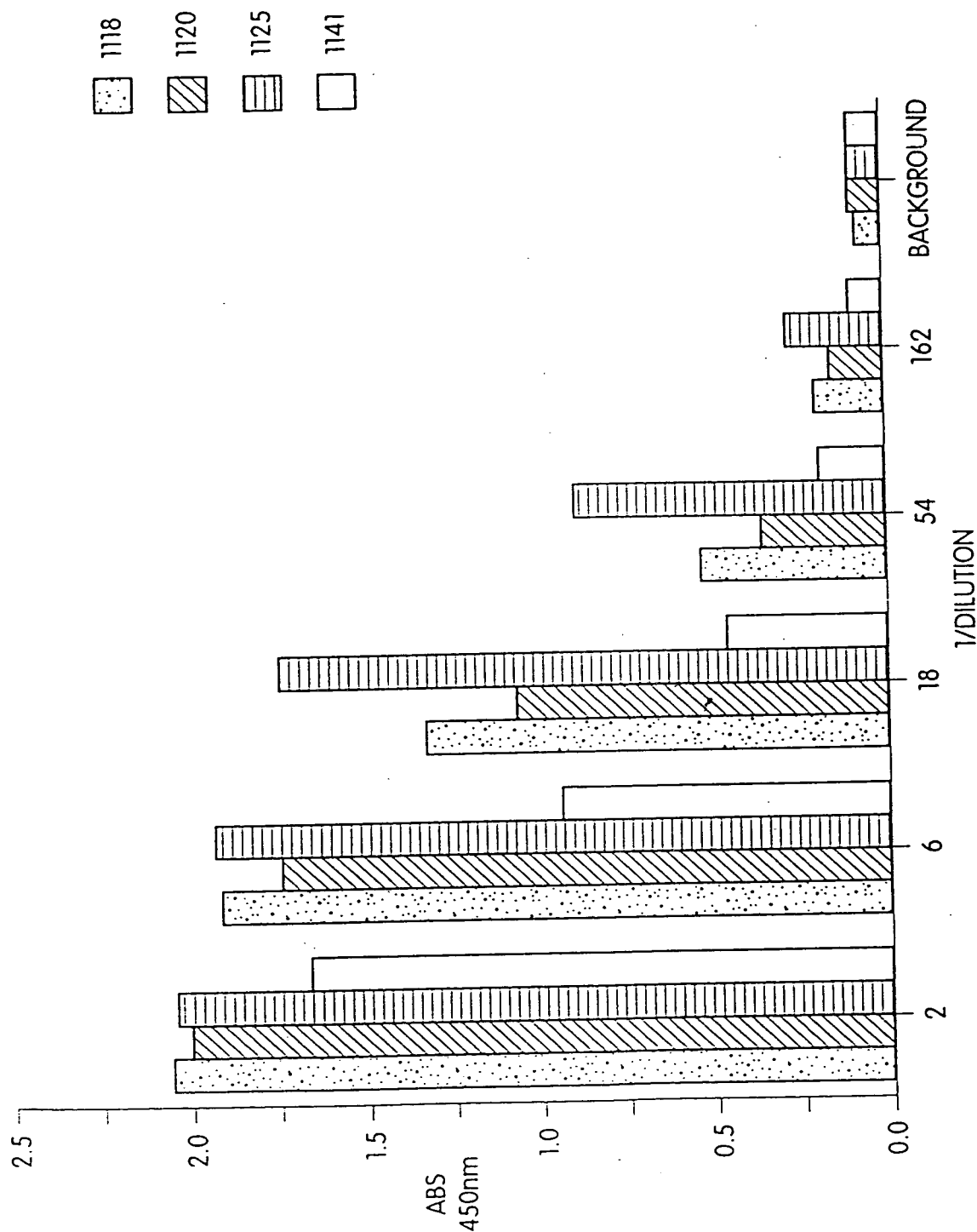


Fig. 9

11/20

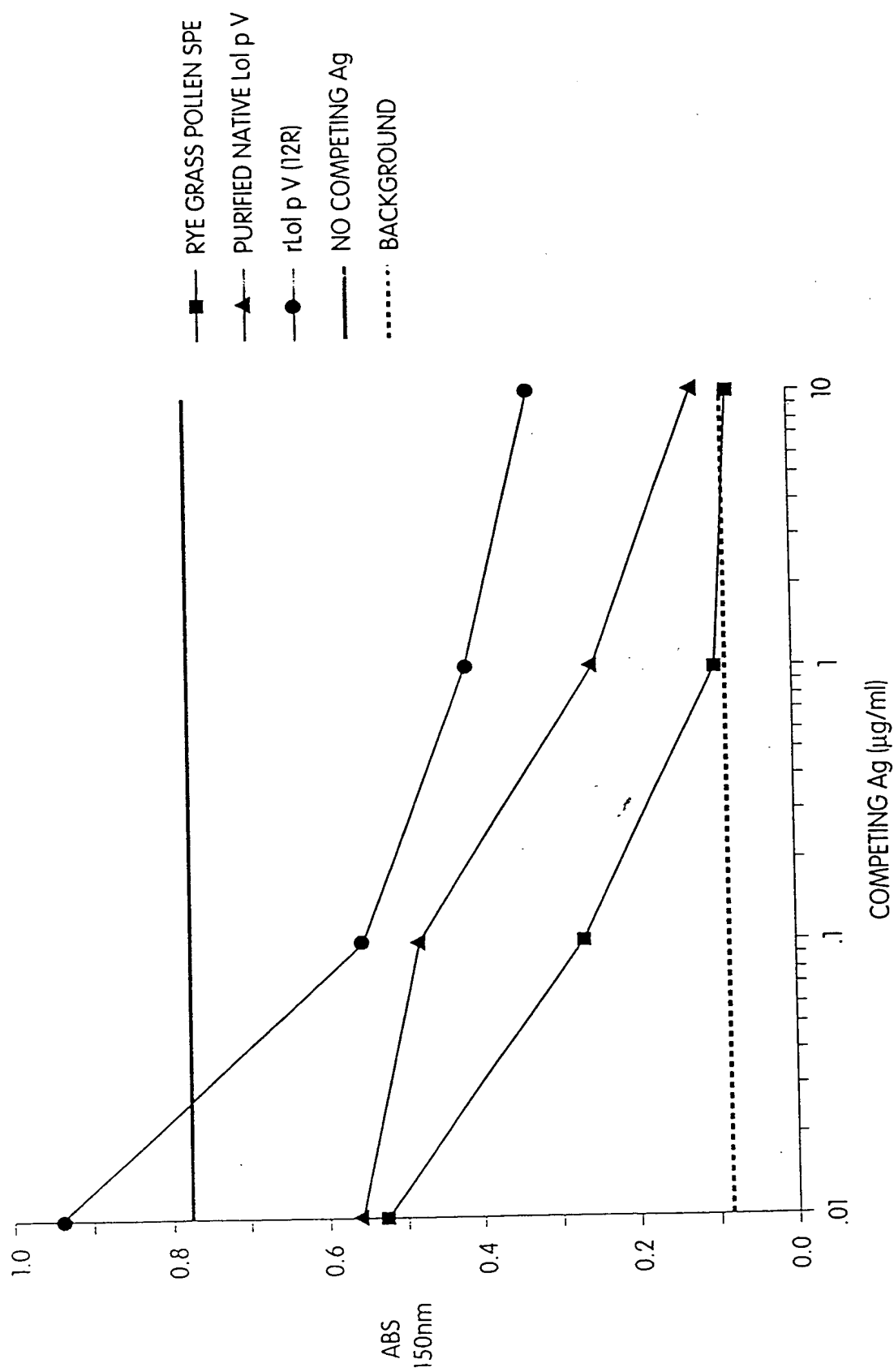


Fig. 10

12/20

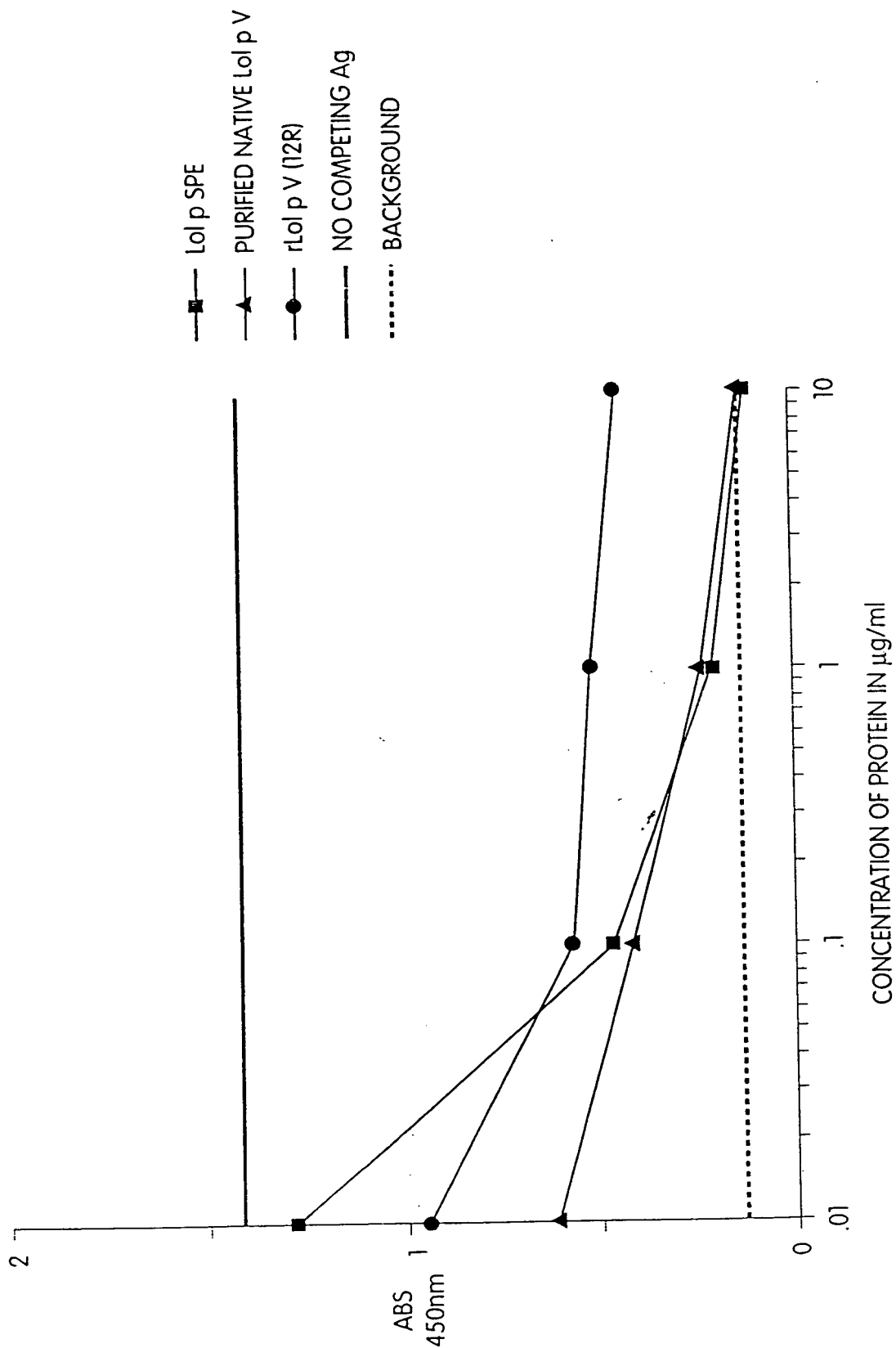


Fig. 11

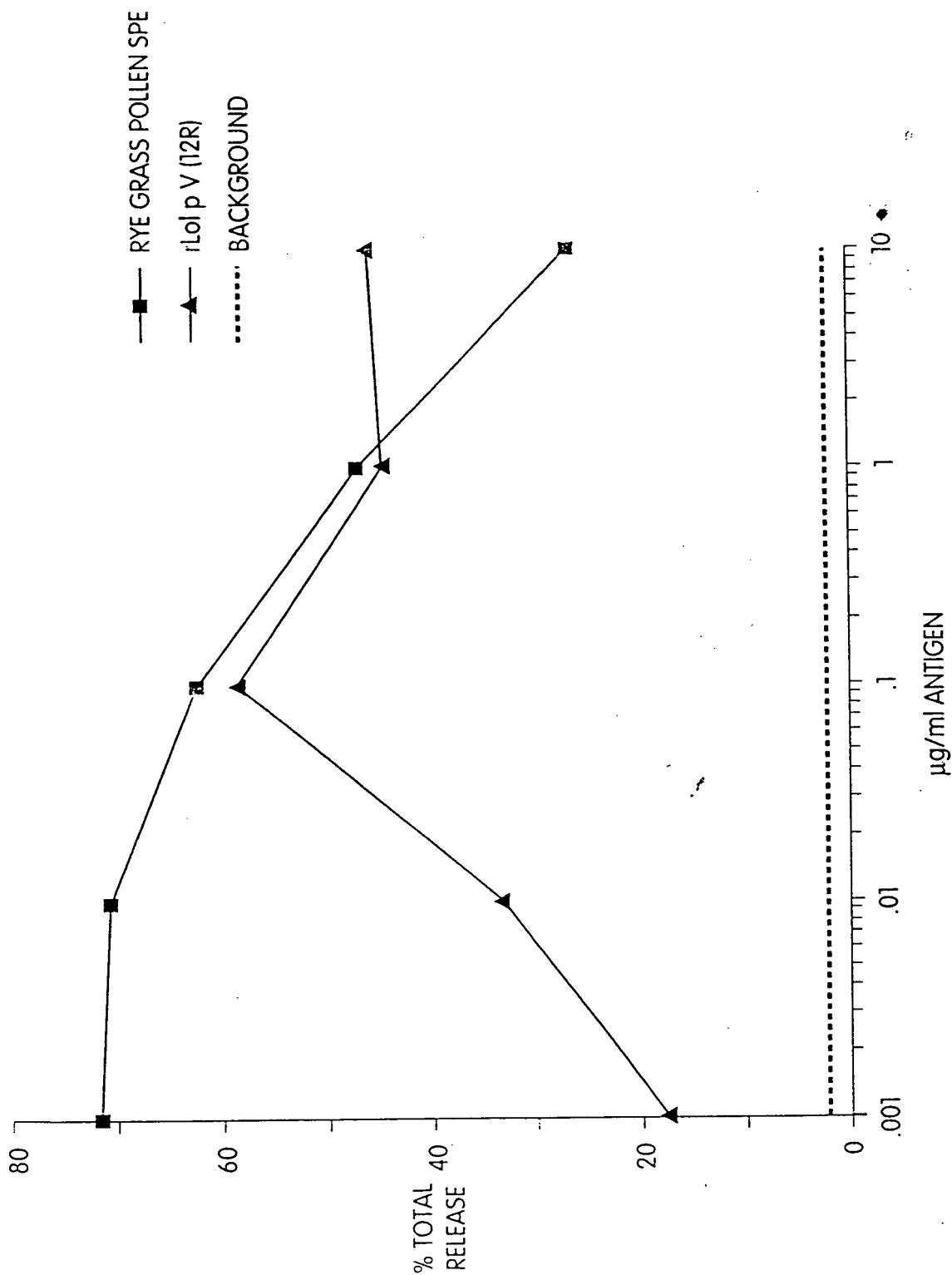


Fig. 12

14/20

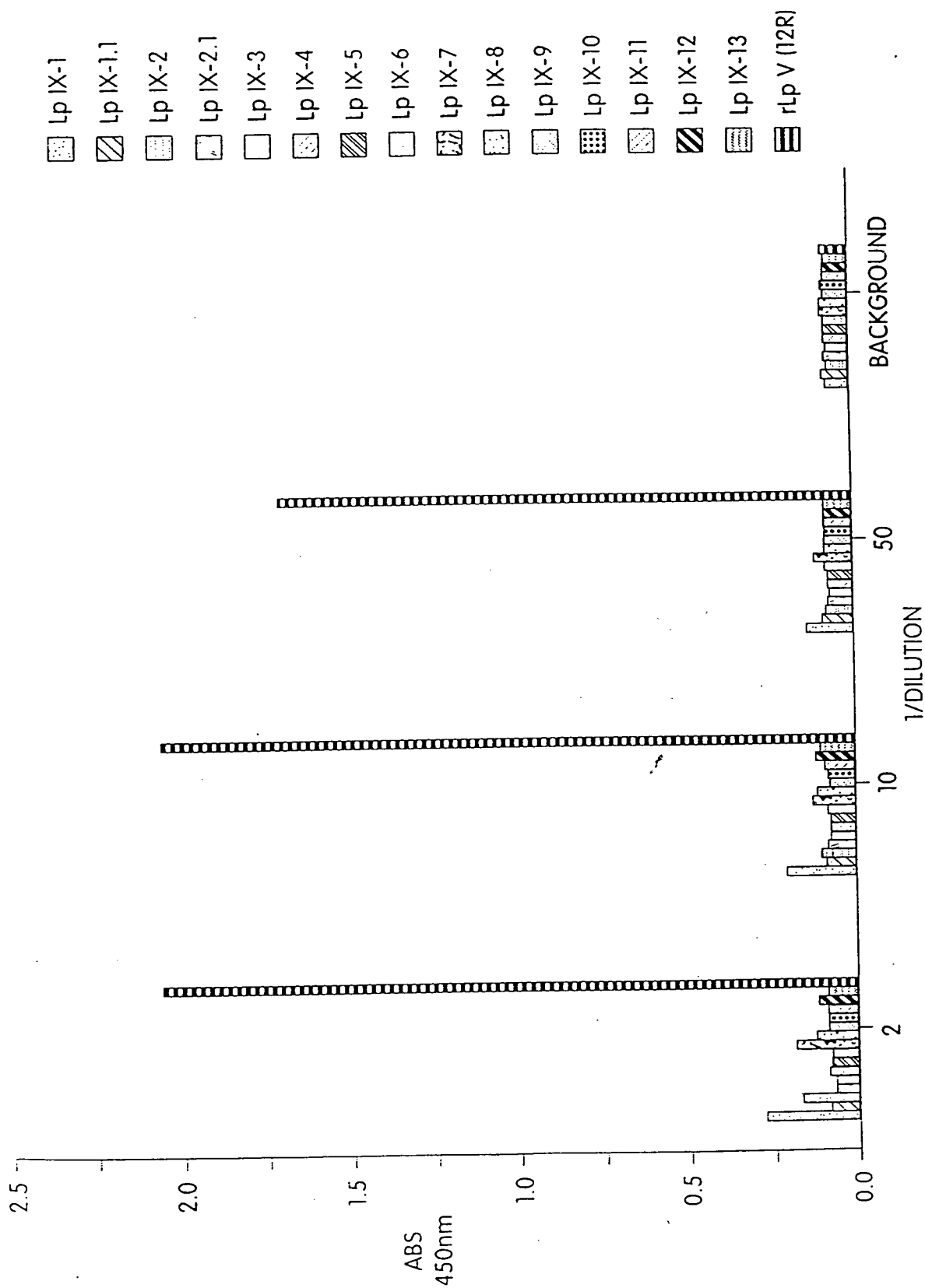


Fig. 13A

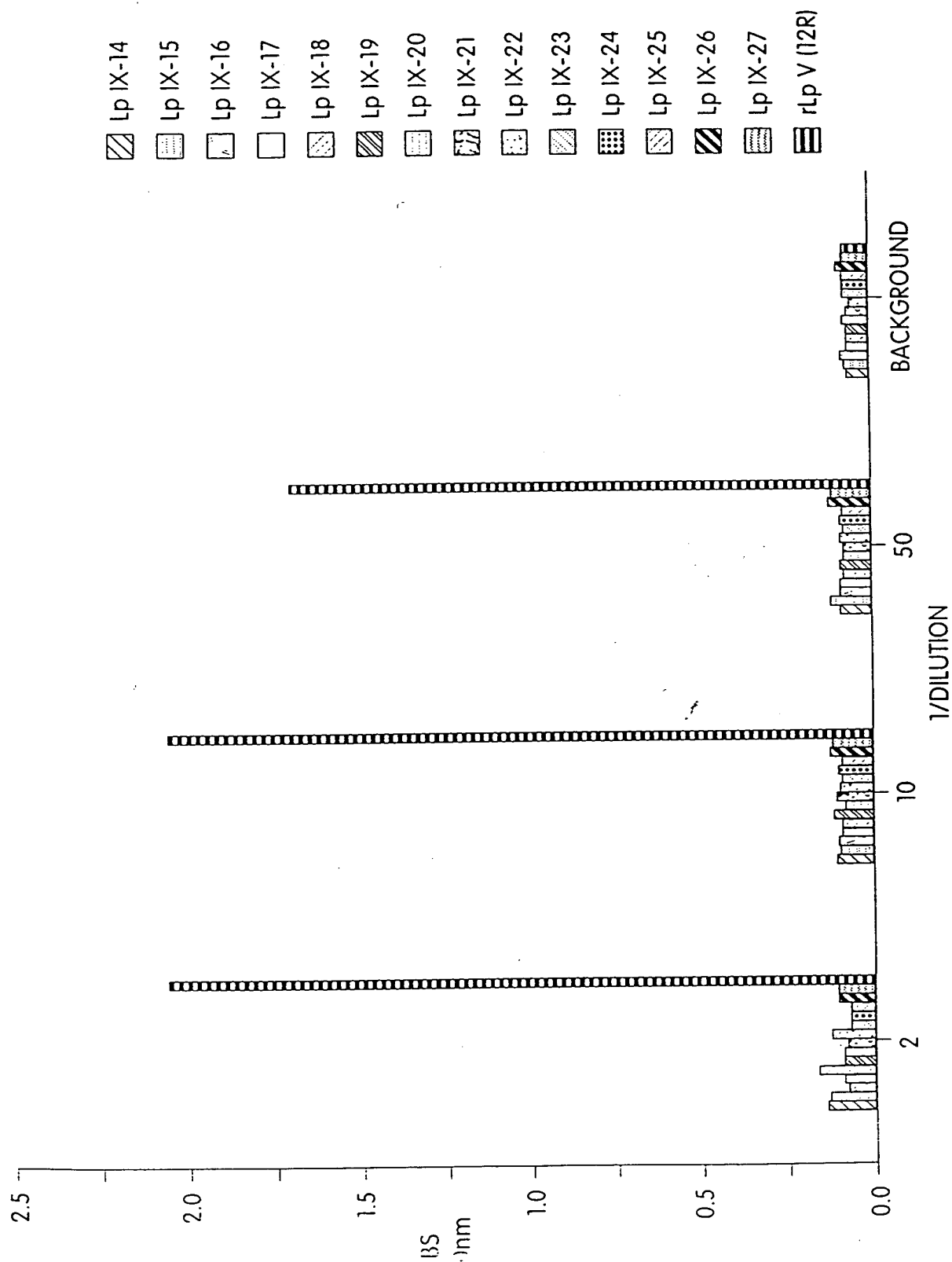


Fig. 13B

16/20

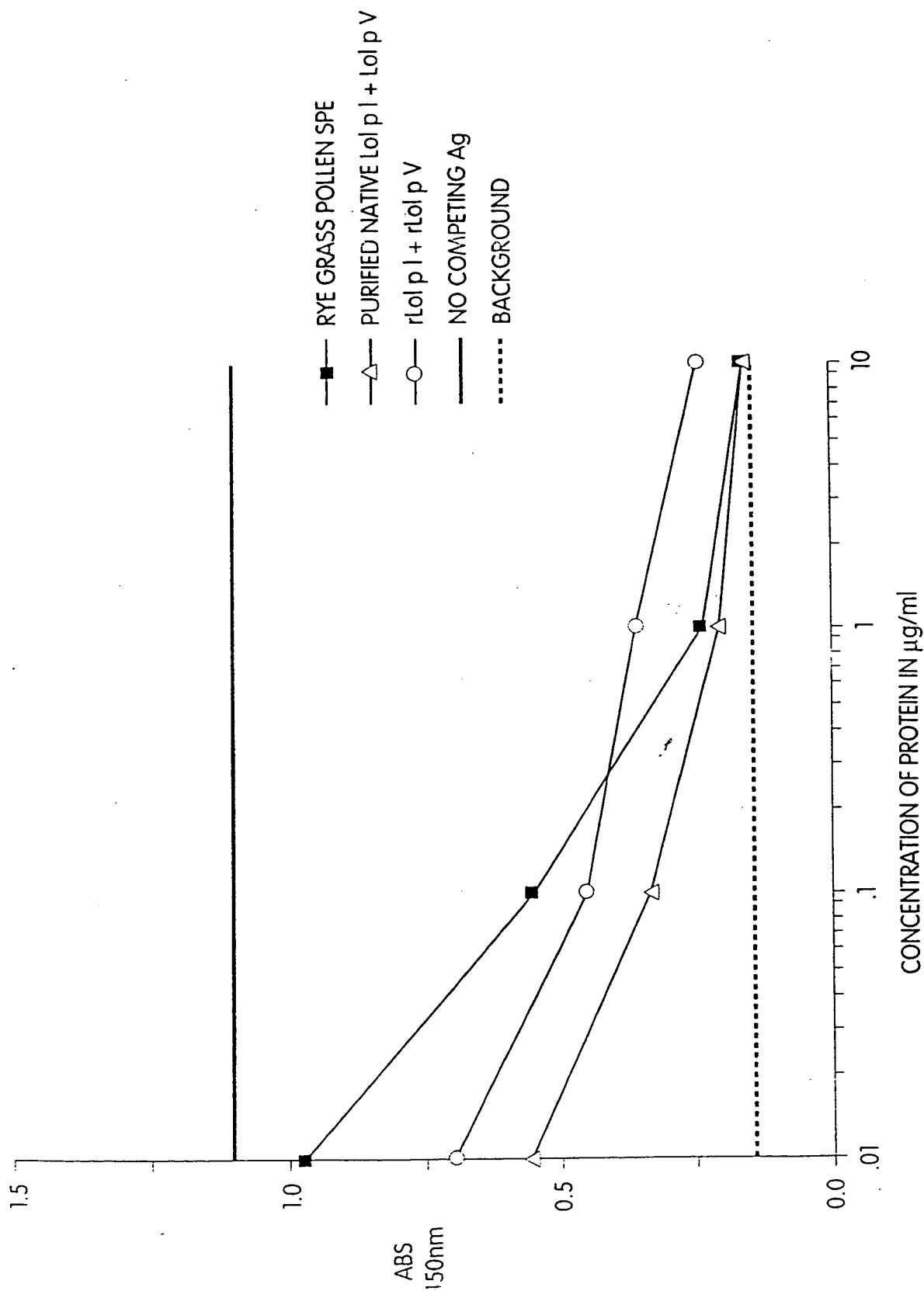


Fig. 14



17/20

200 -  
116.3 -  
97.4 -  
66.3 -  
55.4 -  
  
36.5 -  
31.0 -  
21.5 -

Fig. 15

08/737904-11299

GAATTCGAGGATCCGGGTACCATGGCTCCGACAAACCAACGCAAGAGCAATGGCA 58  
M A  
-24  
TGCAGCAGTACACGGTGGCGCTGTTCTCTGGCCGTGGCCCTCGTGTGGGCCCGCCTCC 118  
V Q Q Y T V A L F L A V A S C R A R A S  
-10  
TACGCCGCGACGCCGGCTACGCCCGCCGCACTCCCGCCACCCCGGCTACCCCGCGGCC 178  
Y A A D A G Y A P A T P A T P A T P A A  
10  
CAGGCGCAGCGTGCCAGCAGGGAAGCGGCGACCCGAGGAGCAGAACTGATCGAGAAG 238  
P G A A V P A G K A A T E E Q K L I E K  
20  
ATCAACGCCGGCTTCAAGGCCCGCGGTGGCGCGCGCGCGGTCCCGCCAGGCGACAAG 298  
I N A G F K A A V A A A A G V P P A D K  
40  
TACAAGACGTTCTCGTAAACCTTCGGCAAGGCTTCAACAAGGCTTCTGGGGACCTC 358  
Y K T F V E T F G K A S N K A F L G D L  
60  
TCGACCAACTACGCCGATGTCAACTCCAGGGCCAGCTCACCTCGAAGCTCGACGCCGC 418  
P T N Y A D V N S R A Q L T S K L D A A  
80  
TACAAGCTGCCCTACGACGCCCGCCAGGCGCCACCCCGAGGCAAGTACGACGCCTAC 478  
Y K L A Y D A A Q G A T P E A K Y D A Y  
100

Fig. 16

538 TCGCCACCCCTCAGCGAGGCGCTCCGCATCATCGCCGGCACCCCTCGAGGTCACGCCGTC  
 V A T L S E A L R I I A G T L E V H A V  
 120  
 598 AGCCCGCTGCCGAGGAGGTCAAGCCCTATCCCGCCGGAGAGCTGCAGATCGTCGACAAG  
 K P A A E E V K P I P A G E L Q I V D K  
 140  
 658 TTGACGTGCGCCTTCAGAACTGCCGCCACCGCCGCCAAGCGCCCGCCCAACGACAAG  
 I D V A F R T A A T A A N A A P T N D K  
 160  
 718 TCACCGTATTCGAGACCACTTTAAAGGCCATCAAGGAGAGCAGCGGGCGGCACCTAC  
 F T V F E T T F N K A I K E S T G G T Y  
 180  
 778 AGAGCTACAAGTTCATTCACCCCTTGAGCGCCGCGTTAAGCAGGCTACGCCGCCACC  
 E S Y K F I P T L E A A V K Q A Y A A T  
 200  
 838 TCGCATCCGGCGGAGGTCAAGTACGCCGCTTTGAGACCGCGCTGAAAAGCGGTC  
 V A S A P E V K Y A V F E T A L K K A V  
 220  
 898 CCGCCATGTCGAGGCCAGAAAGCAAGCCCGCCGCCACCCCGACCCCGCCACC  
 T A M S E A Q K E A K P A T A T P T P T  
 240  
 250

Fig. 16 cont.

CAACTGCCGCGCGGTGGCCACCAAGCCGCCCGCTCGCTGGTGGCTACAAA 958  
 A T A A A V A T N A A P V A A G G Y K  
 260 270  
 TCTGATCAACTCGCTAGCAATATACACATCCATCATGCACATATAGAGCTGTGTATGTA 1018  
 I \*  
 GTGCATGCATGCCGTGGCGCGCAAGTTTGCTCATAATTAATCTTGGTTTTCGTTG 1078  
 TTGCATCCACGAGCGACCGAGCCCGTGGATAGTCGCATGTGTATGTAATTTTCTGAG 1138  
 AATGTGTATATGTAATATATAATTGAGTACTAAAAA 1181

Fig. 16 cont.